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<130> PH-1167

<140> US 09/832,189

<141> 2001-04-11

<150> JP 2000-109954

<151> 2000-04-11

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<170> PatentIn Ver. 2.0

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atgaagaaag ctcatttaaga acagtgggac ccagga atg gaa ctg ctc cac acc 174

Met Glu Leu Leu His Thr
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ttc tgc ggt ggg cgc tgg act ttg ctg ctc ttc acg ggg atc ttg tgc 222
Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu Phe Thr Gly Ile Leu Cys

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ttt gtt gtt gcc cgc gga gtg ggg tat tat ccc agg ttc tct cca ttc 270
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ttt ttc ctt tgc act cat cat gga gaa ctg gaa gga gat ggg gaa caa 318
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gga gaa gtg ctc atc tct ctg cac ctg gcg ggc aac ccc agc tac tac 366
 Gly Glu Val Leu Ile Ser Leu His Leu Ala Gly Asn Pro Ser Tyr Tyr
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gac cgt cag ttt ggt acc cag ttt atg tgc agt gtc gtt gct tcc cac 558
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gag cag tgt ggt gca att atg cat ggt ggg gca gtc act ttt tgt gat 894
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agt tgg atg cca ttg gag aga att agt gct cct tcc aat gtt agc acc 1086
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Glu Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Leu Ala
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Gly Asn Pro Ser Tyr Tyr Ile Pro Gly Gln Glu Tyr His Val Thr Ile
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115 120 125
Ser Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser
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Ala Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala
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Gln Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro
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Asn Leu Ala Glu Ile His Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe
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Asp Ser Tyr Lys Leu Gln Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys
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Arg Asn Cys Glu Val Gly Glu Gln Cys Gly Ala Ile Met His Gly Gly
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245 250 255
Gln Met Asn Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser
260 265 270
Gly Ser Cys Arg Phe Ser Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr
275 280 285
Thr Lys Asn Asn Ser Ser Ser Trp Met Pro Leu Glu Arg Ile Ser Ala
290 295 300

Pro Ser Asn Val Ser Thr Ile Ile His Ile Ile Tyr Leu Pro Pro Glu
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Ala Lys Gly Glu Asn Val Lys Phe Arg Trp Arg Gln Glu Asn Met Gln
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Ala Gly Asp Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile
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Ile Asn Ala Ala His Lys Glu Val Val Leu Glu Asp Asn Leu Asp Pro
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370 375 380

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Met Glu Arg Gly
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 Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala Lys Asn Asn Thr
 280 285 290

gct gat tgg att cag ctg gag aaa att aga gcc cct tcc aat gtg agc 1206
 Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro Ser Asn Val Ser
 295 300 305

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 Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala Lys Gly Glu Ser
 310 315 320

gtg cag ttc cag tgg aaa cag gac agc ctg cga gtg ggt gag gtg tat 1302
 Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val Gly Glu Val Tyr
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gag gcc tgc tgg gcc ctg gat aac atc ctg gtc atc aat tca gcc cac 1350
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aga gaa gtc gtt ctg gag gac aac ctc gac ccg gtc gac acg ggc aac 1398
 Arg Glu Val Val Leu Glu Asp Asn Leu Asp Pro Val Asp Thr Gly Asn
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tgg ctc ttc ttc cct gga gca acg gtc aag cat agc tgt cag tca gat 1446
 Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His Ser Cys Gln Ser Asp
 375 380 385

ggg aac tcc att tat ttc cat gga aat gaa ggc agc gag ttc aat ttt 1494
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tgg tca gaa gaa ttt gag agc cag ccc aca gga tgg gat atc ttg gga 1590
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 Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser Ile Asn Leu Gly
 565 570 575 580
 tgc ggc aca cac cag cct ggg aac agg tga gaagcatgcc gagtgtccata 2072
 Cys Gly Thr His Gln Pro Gly Asn Arg
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 35 40 45

Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly
 50 55 60

Asn Pro Thr Tyr Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser
 65 70 75 80

Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser
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85

90

95

Thr Ser Ile Gln Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly
 100 105 110

Phe Gly Ile Met Ser Asp His Gln Phe Gly Asn Gln Phe Met Cys Ser
 115 120 125

Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe
 130 135 140

Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala
 145 150 155 160

Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln
 165 170 175

Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Thr Ala Tyr Ser His
 180 185 190

Leu Ala Glu Ile His Ser Asp Ser Val Ile Leu Arg Asp Asp Phe Asp
 195 200 205

Ser Tyr Gln Gln Leu Glu Leu Asn Pro Asn Ile Trp Val Glu Cys Ser
 210 215 220

Asn Cys Glu Met Gly Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala
 225 230 235 240

Val Thr Phe Cys Glu Pro Tyr Gly Pro Arg Glu Leu Thr Thr Cys
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Leu Asn Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly
 260 265 270

Ser Cys Arg Phe Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala
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Lys Asn Asn Thr Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro
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Ser Asn Val Ser Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala
 305 310 315 320

Lys Gly Glu Ser Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val
 325 330 335

Gly Glu Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Val Ile
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Asn Ser Ala His Arg Glu Val Val Leu Glu Asp Asn Leu Asp Pro Val
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Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His Ser
 370 375 380

Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Asn Glu Gly Ser
 385 390 395 400

Glu Phe Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Thr Glu Asp
 405 410 415

Ile Gln Glu Gln Trp Ser Glu Glu Phe Glu Ser Gln Pro Thr Gly Trp
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Asp Ile Leu Gly Ala Val val Gly Ala Asp Cys Gly Thr Val Glu Ser
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Gly Leu Ser Leu Val Phe Leu Lys Asp Gly Glu Arg Lys Leu Cys Thr
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Pro Tyr Met Asp Thr Thr Gly Tyr Gly Asn Leu Arg Phe Tyr Phe Val
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Leu Tyr Ala Lys Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr
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Ser His Gln Gly Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His
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Artificial Sequence

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Artificial Sequence

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